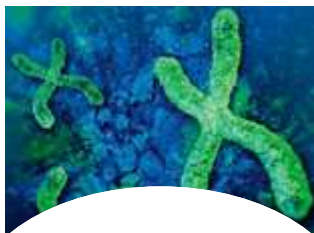




Betterave2020



Bruno Desprez
Venise, I

19th June 2018



Financed by



AKER Programme – For a competitive innovation

Progress made since the last meeting

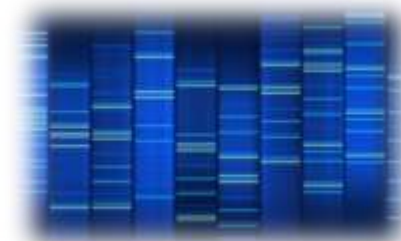


Participants of the fourth joint meeting of the ECPGR working group on Beta and the WBN, 20-22 June 2012, Cappelle-en-Pévèle, France
(photo: company Florimond Desprez)



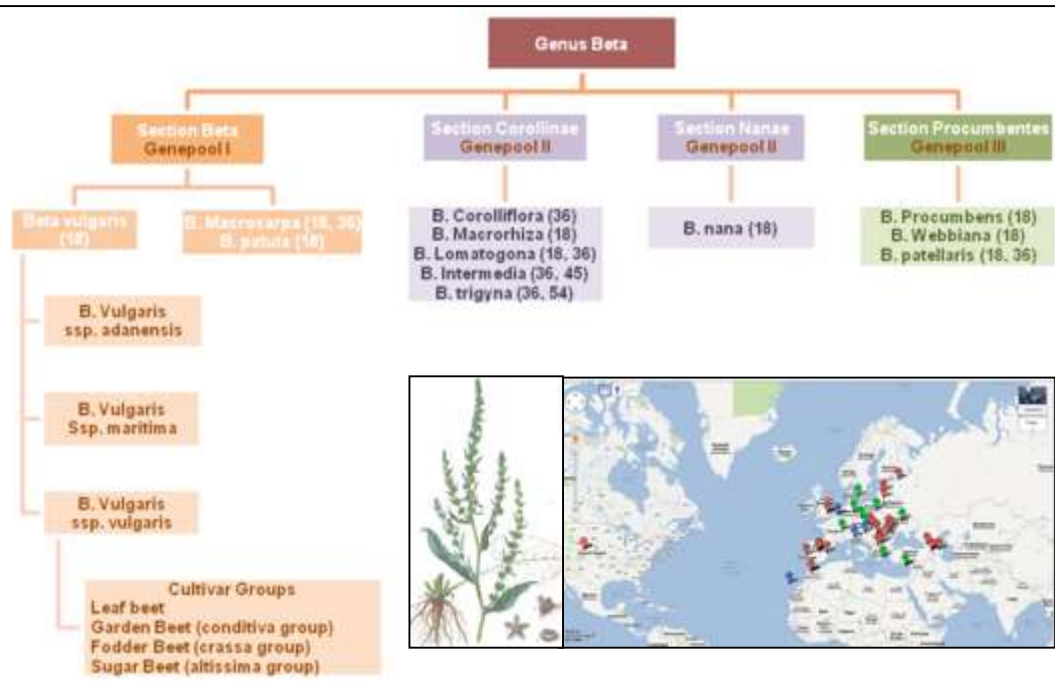
Introduction

1. AKER strategy
2. AKER 's results
3. AKER's partnerships and discussion



Conclusions

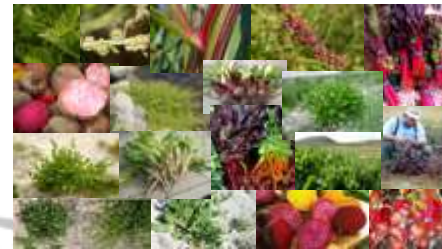
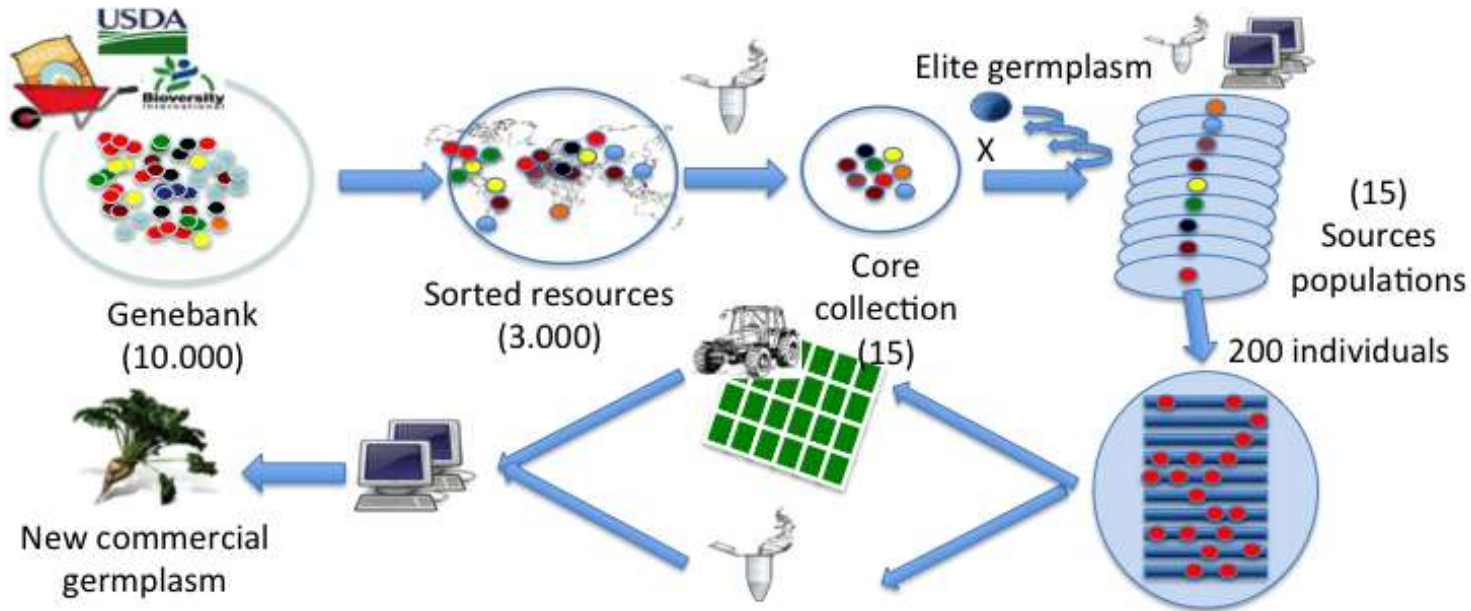
- Genetic resources available in the genus *Beta*.
 - Only accessions from the Group I 46 genebanks

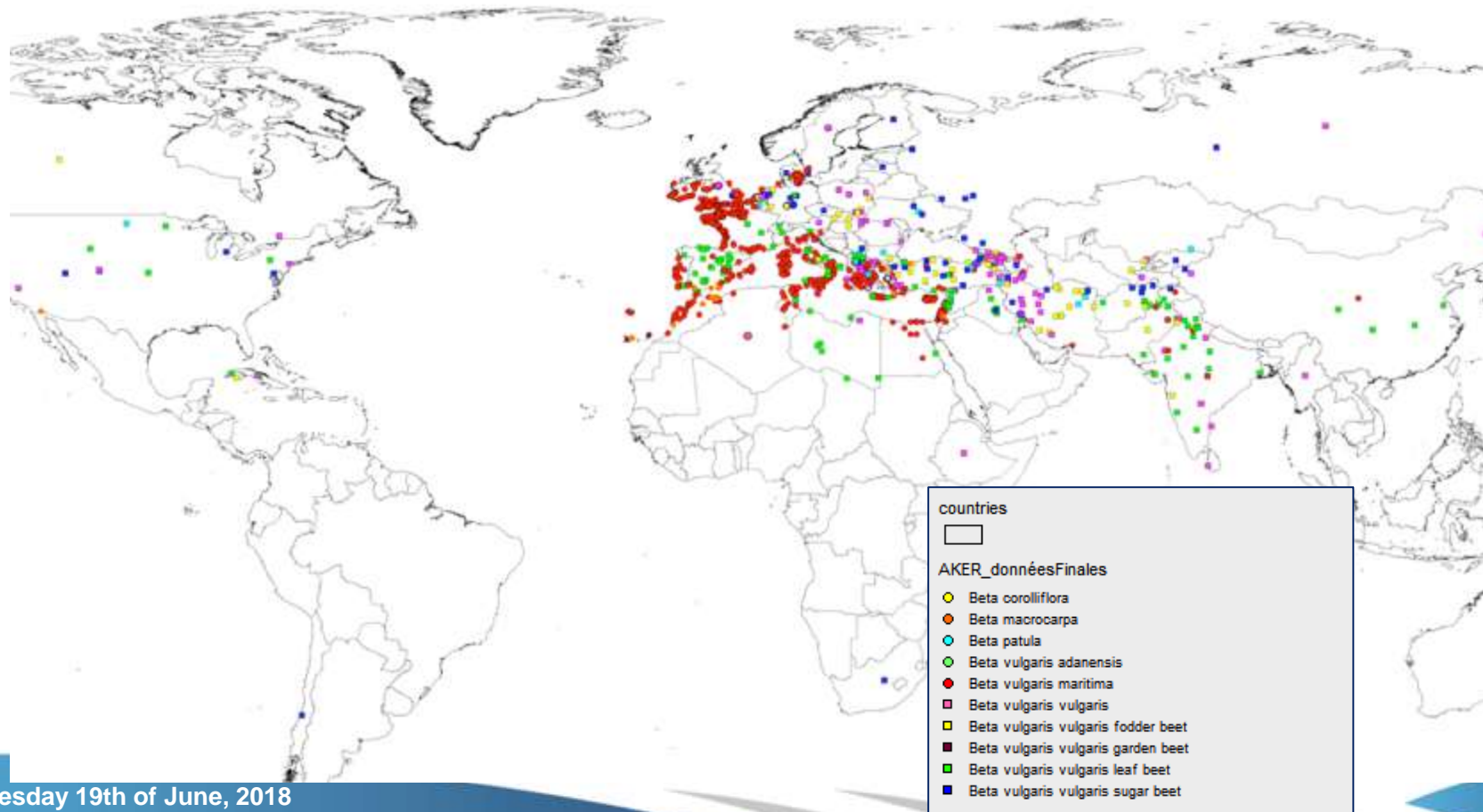


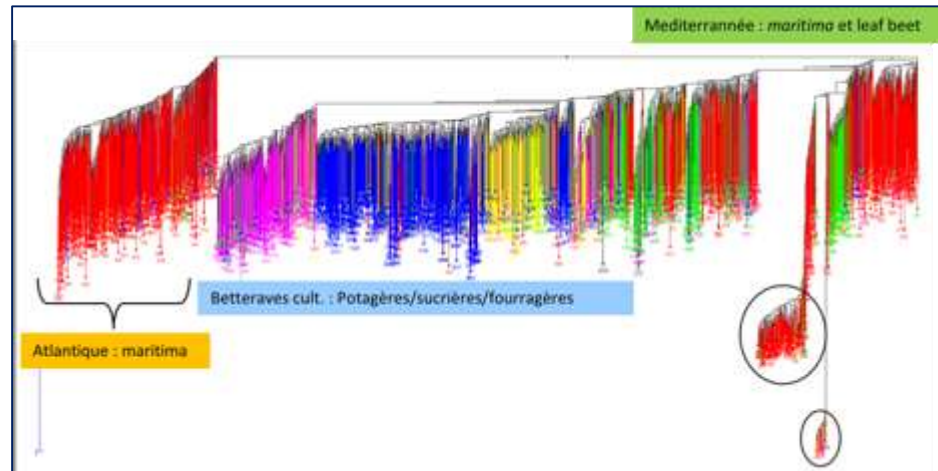
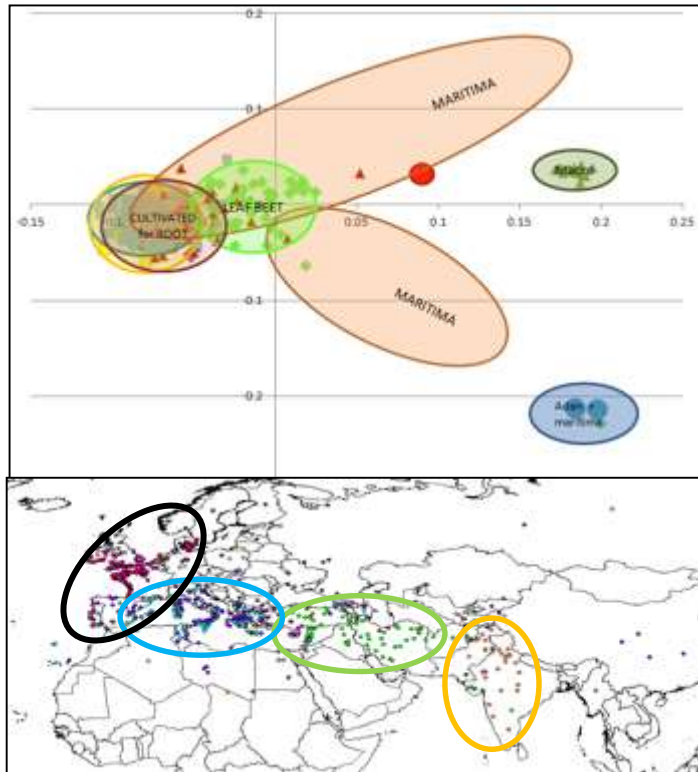
Réf. *Beta maritima*, the origin of beet,
E. Biancardi, L. W. Panella, R.T. Lewellen, 2012



Betterave2020







40 ACCESSIONS representing 100% of the total allelic variation

15 ACCESSIONS representing 100% of all allelic variation not included in the allelic richness of elite germplasm

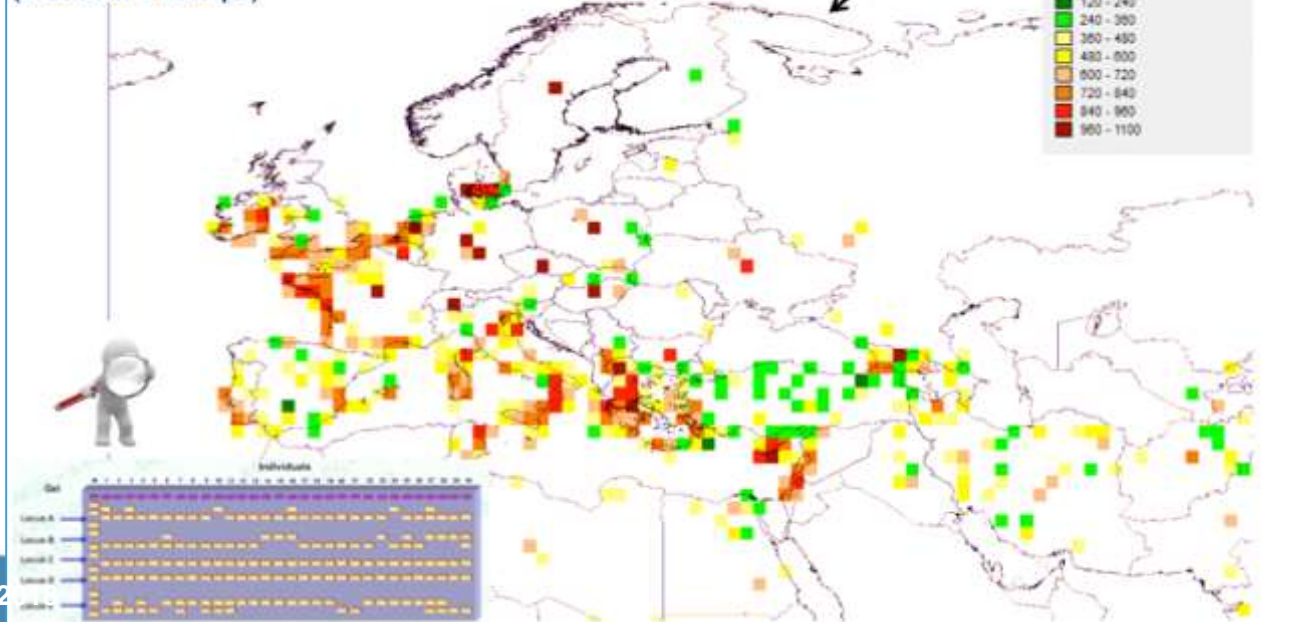
Representation of the DAPC clusters on the map
(*B. macrocarpa* and *B. adanensis* were discarded because of their strong distance from other groups)



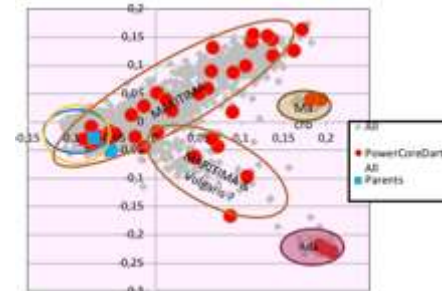
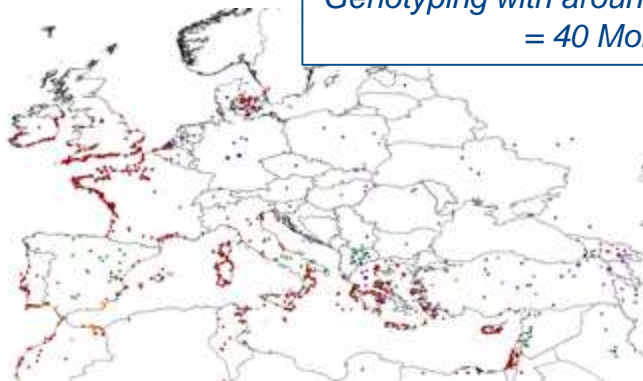
Betterave2020

Construction de la Collection de Référence

Richesse allélique
(Zoom sur l'Europe)



*Genotyping with around 2 Mio SNPs and 38 Moi DArTs
= 40 Moi Mol. Marker Data*



Karine Henry, AKER Sc. Coord.
"The 15 accessions cover 100% of the variability"

3,000 accessions collection from 46 genebanks
Selection of 15 accessions based on the diversity analysis

AKERdatasfinal_22mai13

- ◆ Beta macrocarpa
- Beta patellaris
- Beta patula
- Beta sp.
- Beta vulgaris subsp. adanensis
- Beta vulgaris subsp. maritima
- Beta vulgaris subsp. vulgaris
- Beta vulgaris vulgaris elite
- Beta vulgaris vulgaris elite HD
- Beta vulgaris vulgaris fodder b
- Beta vulgaris vulgaris garden b
- Beta vulgaris vulgaris leaf beet
- Beta vulgaris vulgaris sugar be



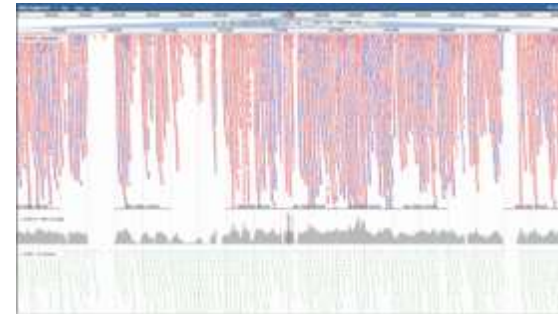
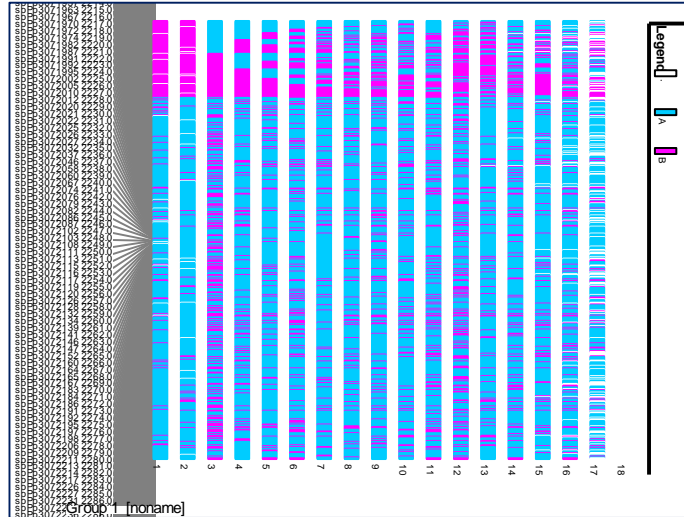
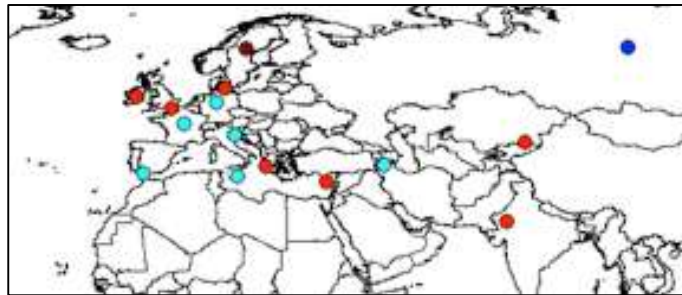
	%	ch
-	0.0	18.1
A	89.1	113843.9
B	3.7	4748.3
H	7.2	9205.8

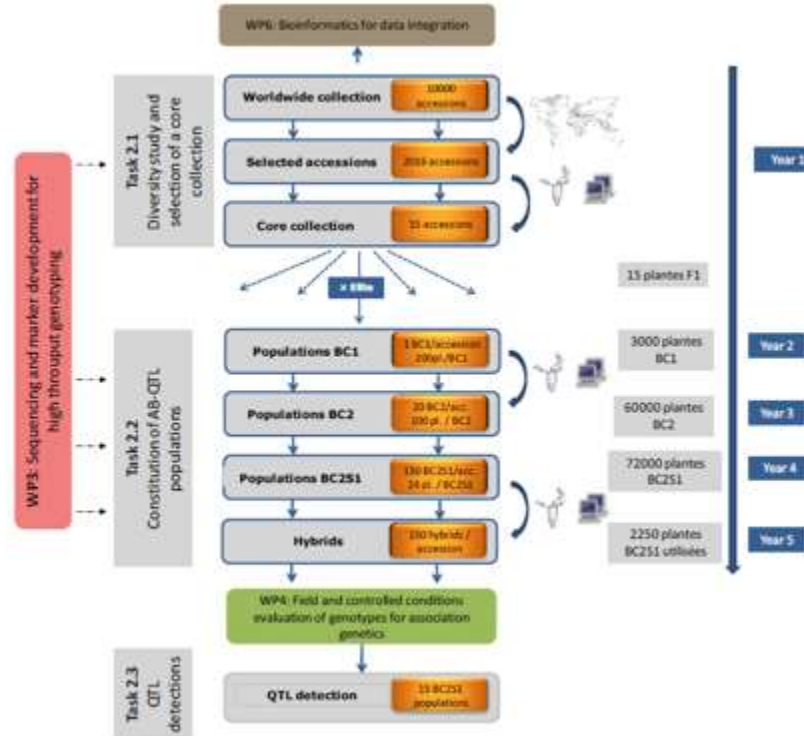


CORE COLLECTION



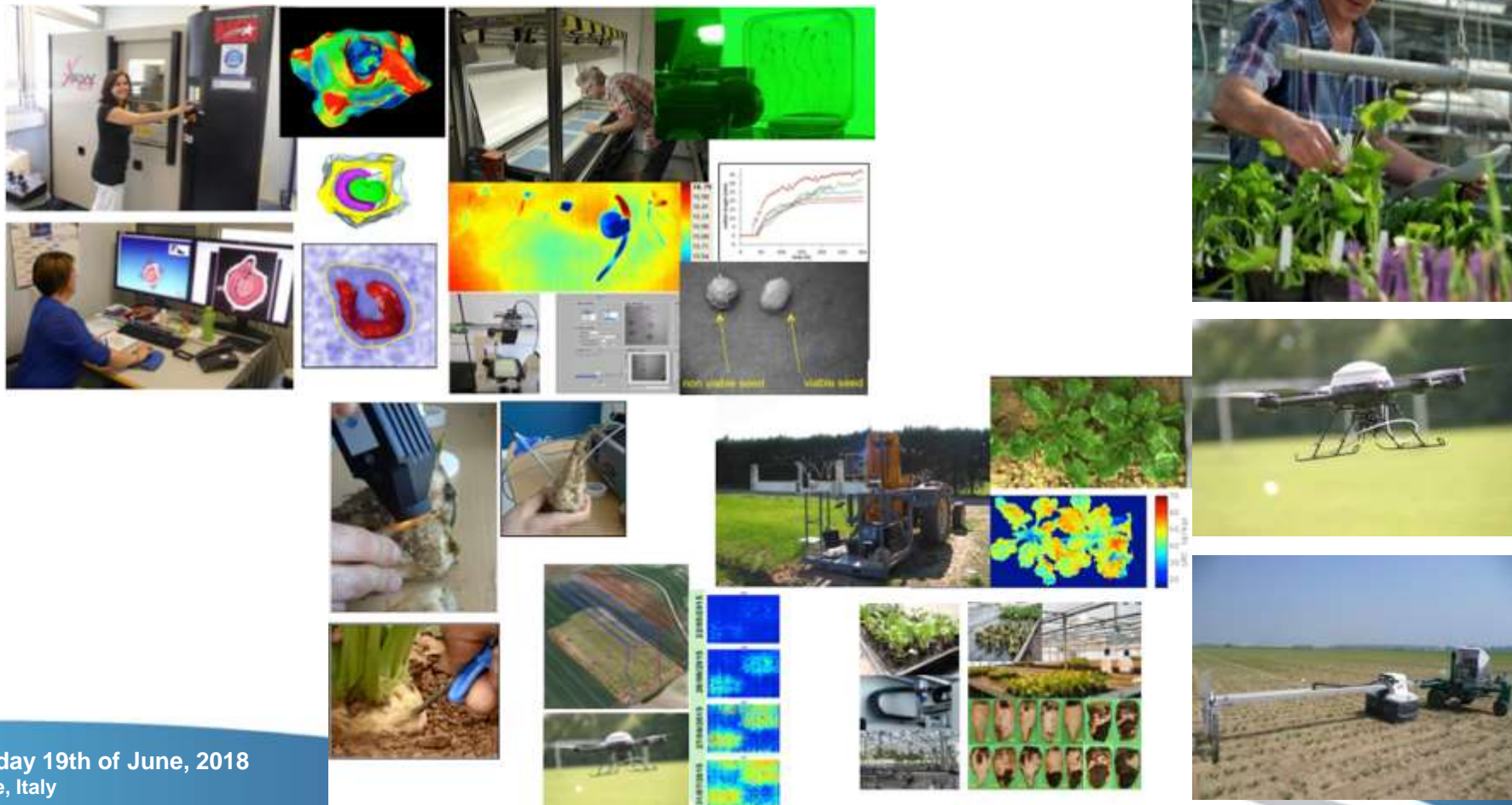
Betterave2020







Nr_plants	μ (segment)	max (segm)	min (segm)
28	3,6	8	2
198	3,1	8	1





<https://urgi.versailles.inra.fr/ephep/ephep/ontologyportal.do>

<https://ais.florimond-desprez.fr/ephep/ephep/ontologyportal.do>

http://www.cropontology.org/ontology/CO_333/Beet%20Ontology

Beet Ontology (v 1.0) August 2017



Germplasm

Reset tab

Search by genus *

Search by crop *

Search by germplasm *

Search by panel, collection or population *

* Only the first terms corresponding to the current search are suggested.

Selected accessions preview

Only the first 10000 results can be previewed

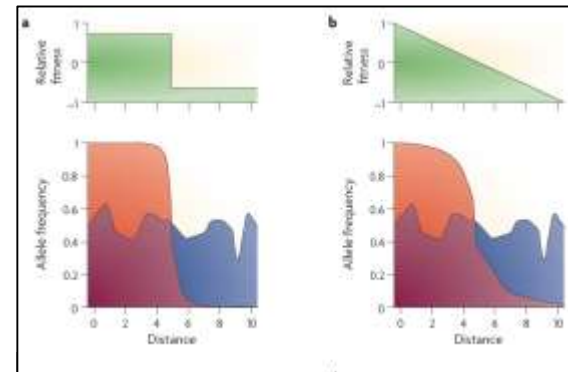
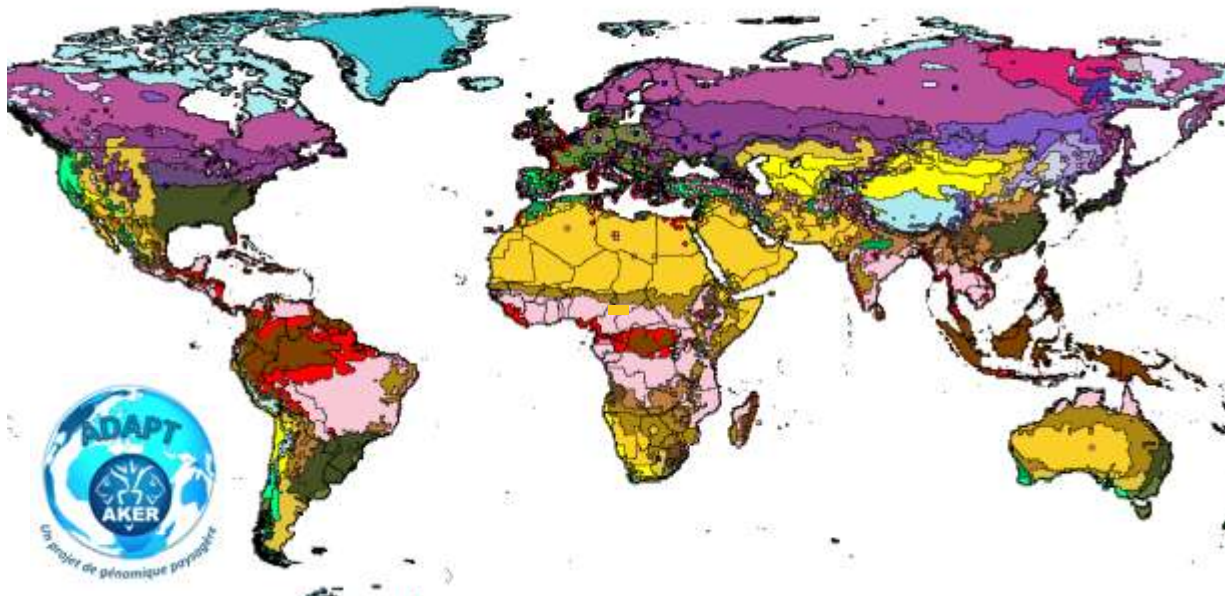
1-10 of 10,630

Accession number	Accession name	Taxon name
BETA_863	AKER_1141	Patellifolia patellaris
BETA_882	AKER_385	Patellifolia patellaris
BETA_895	AKER_1398	Patellifolia patellaris
BETA_887	AKER_394	Patellifolia patellaris
BETA_862	AKER_392	Patellifolia patellaris
BETA_894	AKER_1397	Patellifolia patellaris
BETA_419	AKER_413	Patellifolia procumbens
IDBBNR_731	AKER_6728	Patellifolia webbiana
IDBBNR_727	AKER_383	Patellifolia patellaris
NC063758	AKER_407	Patellifolia patellaris

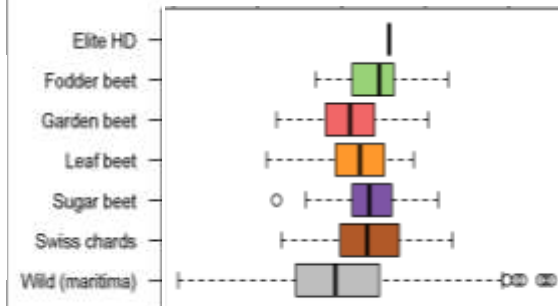
Landscape genetic – Accession distribution and eco-geographical zonation

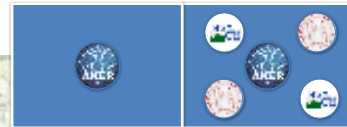


Betterave2020

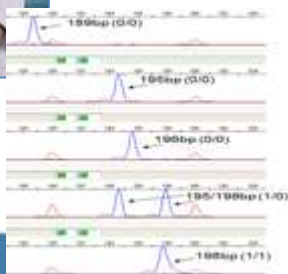
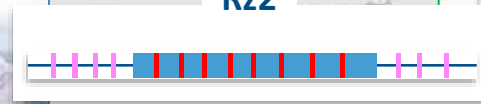


Neutral allele (blue) Advantageous allele (red)





Betterave2020



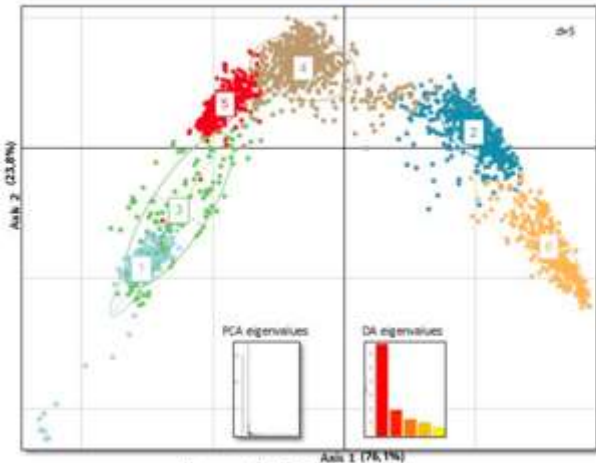
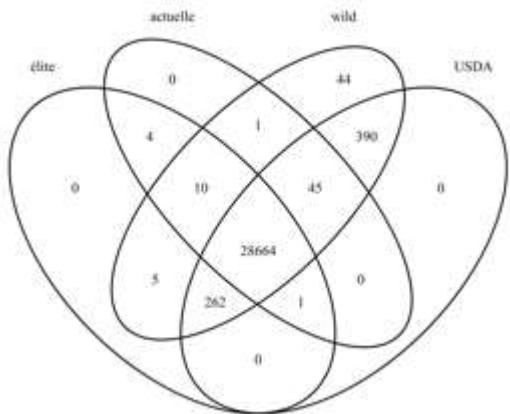
Type	Name	Accession	Date	Status	Description
...
...
...



Genetic structure in the global population: a more precise genetic differentiation



Betterave2020



Board 2 : Cluster compositions

Cluster	Elites	Wild	Current varieties	USDA	TOTAL
Cluster1	2%	0%	96%	2%	100%
Cluster2	0%	99.7%	0%	0.3%	100%
Cluster3	93%	0%	0%	7%	100%
Cluster4	19%	16%	4%	70%	100%
Cluster5	4.7%	0.3%	80%	15%	100%
Cluster6	0%	100%	0%	0%	100%

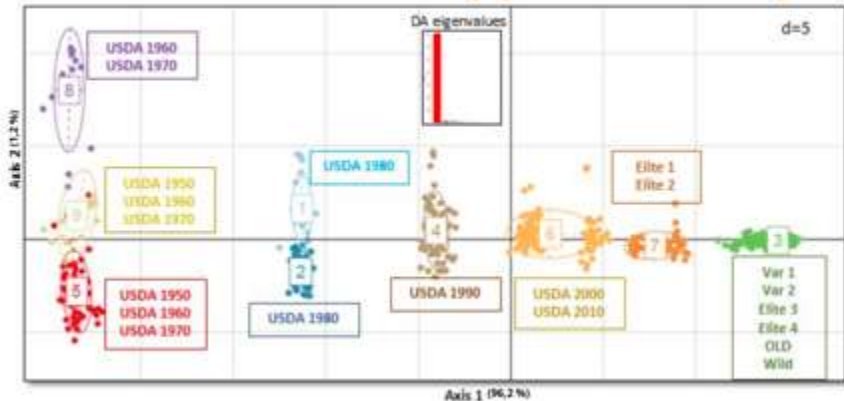
- 1st axis : Wild accessions are far from current varieties and elite lines
⇒ Elite lines and current varieties are close
- Cluster 1 : Some distinct accessions
Cluster 3 : Diversity for a lot of elite lines
- 2nd axis : USDA accessions "make a link" between many wild accessions and many current varieties
2 "pools" of current varieties joined by elite lines



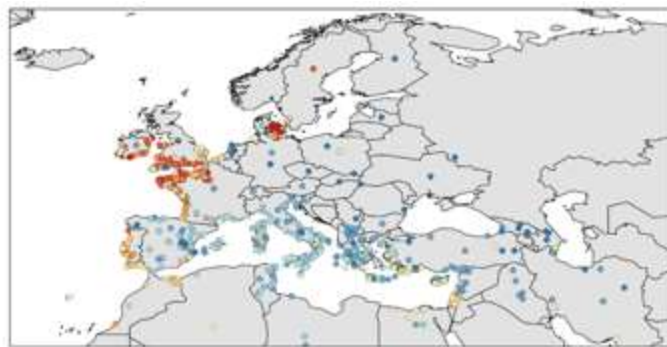
Be Domino



Genetic differentiation in the different subpopulations selected: temporal analysis



- 390 alleles (USDA-wild)
- 0.0000 - 49.0000
 - 49.0000 - 98.0000
 - 98.0000 - 147.0000
 - 147.0000 - 196.0000
 - 196.0000 - 245.0000
 - 245.0000 - 294.0000
 - 294.0000 - 343.0000
 - 343.0000 - 392.0000
 - 392.0000 - 441.0000
 - 441.0000 - 490.0000





ANR – 11 – BTBR - 0007

Soutenu par

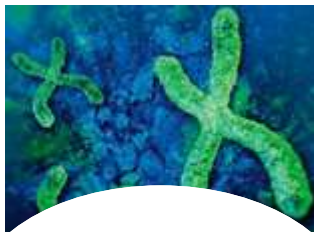


Vers une sélection de précision...

<http://www.aker-betterave.fr>



Betterave2020



European
Cooperative
Programme
for Plant
Genetic
Resources

ECP/GR

Bruno Desprez
Venise, I

19th June 2018



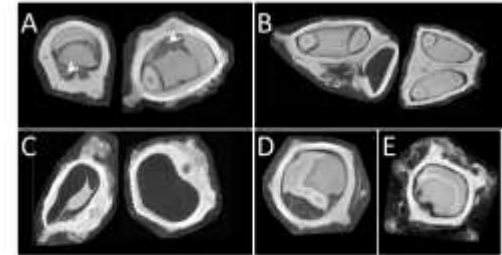
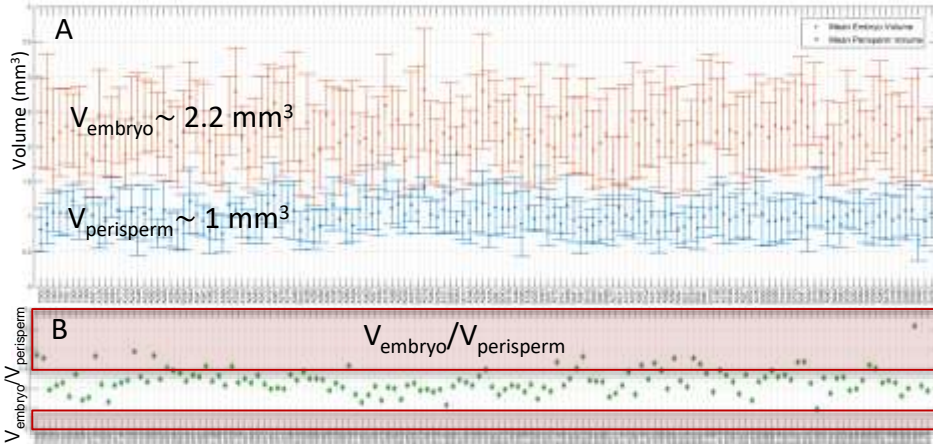
Thank you for
your attention !





Betterave2020

Results on the pilot population (PP) : Embryo and perisperm volumes for different genotypes



Particular cases causing image processing failure : (A) Necrotic aspect; (B) Multi-germ seeds; (C) Empty seeds; (D) Embryo malformation; (E) Unbrushed/badly brushed seeds

Results on the pilot population (PP) : Seed Coat volumes for different genotypes

